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RAW SEQUENCE LISTING

DATE: 02/21/2002

PATENT APPLICATION: US/09/824,322B

TIME: 12:39:05

Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I824322B.raw

ENTER ID

3 <110> APPLICANT: Baker, Brenda
 4 Bennett, C. Frank
 5 Butler, Madeline M.
 6 Shanahan, William R.
 8 <120> TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS
 FACTOR-ALPHA (TNF-
 9 ALPHA) EXPRESSION
 11 <130> FILE REFERENCE: ISPH-0501
 13 <140> CURRENT APPLICATION NUMBER: US 09/824,322B
 14 <141> CURRENT FILING DATE: 2001-04-02
 16 <150> PRIOR APPLICATION NUMBER: US 09/313,932
 17 <151> PRIOR FILING DATE: 1999-05-18
 19 <150> PRIOR APPLICATION NUMBER: US 09/166,186
 20 <151> PRIOR FILING DATE: 1998-10-05
 22 <160> NUMBER OF SEQ ID NOS: 503
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 3634
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
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 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (796..981,1589..1634,1822..1869,2171..2592)
 33 <220> FEATURE:
 34 <221> NAME/KEY: exon
 35 <222> LOCATION: (615)..(981)
 37 <220> FEATURE:
 38 <221> NAME/KEY: intron
 39 <222> LOCATION: (982)..(1588)
 41 <220> FEATURE:
 42 <221> NAME/KEY: exon
 43 <222> LOCATION: (1589)..(1634)
 45 <220> FEATURE:
 46 <221> NAME/KEY: intron
 47 <222> LOCATION: (1635)..(1821)
 49 <220> FEATURE:
 50 <221> NAME/KEY: exon
 51 <222> LOCATION: (1822)..(1869)
 53 <220> FEATURE:
 54 <221> NAME/KEY: intron
 55 <222> LOCATION: (1870)..(2070)
 57 <220> FEATURE:
 58 <221> NAME/KEY: exon
 59 <222> LOCATION: (2171)..(3381)
 61 <300> PUBLICATION INFORMATION:

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62 <301> AUTHORS: Nedwin, G.E.
 63 Naylor, S.L.
 64 Sakaguchi, A.Y.
 65 Smith, D.
 66 Jarrett-Nedwin, J.
 67 Pennica, D.
 68 Goeddel, D.V.
 69 Gray, P.W.

70 <302> TITLE: Human lymphotoxin and tumor necrosis factor genes: structure, homology
 and

71 chromosomal localization
 72 <303> JOURNAL: Nucleic Acids Res.
 73 <304> VOLUME: 13
 74 <305> ISSUE: 17
 75 <306> PAGES: 6361-6373
 76 <307> DATE: 1985-09-11
 77 <308> DATABASE ACCESSION NO: X02910 Genbank
 78 <309> DATABASE ENTRY DATE: 1997-02-17
 80 <400> SEQUENCE: 1
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 83 tcctgaggcc tcaagcctgc caccaagccc ccagctcctt ctccccgcag gacccaaaca 120
 85 caggcctcag gactcaacac agcttttccc tccaaccogt tttctctccc tcaacggact 180
 87 cagctttctg aagccctcc cagttctagt tctatctttt tcctgcatcc tgtctggaag 240
 89 ttagaaggaa acagaccaca gacctggtcc ccaaaagaaa tggaggcaat aggttttgag 300
 91 gggcatggg acggggttca gctccaggg tcctacacac aaatcagtca gtggcccaga 360
 93 agacccccct cggaatcgga gcagggagga tggggagtgt gaggggtatc cttgatgctt 420
 95 gtgtgtcccc aactttccaa atccccgccc ccgcgatgga gaagaaaccg agacagaagg 480
 97 tgcagggcc actaccgctt cctccagatg agctcatggg tttctccacc aaggaagttt 540
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 101 ttgttgccac acccagccag cagacgctcc ctacgcaagg acagcagagg accagctaag 660
 103 agggagagaa gcaactacag accccccctg aaaacaaccc tcagacgcca catccccga 720
 105 caagctgcca ggcaggttct ctctctctca catactgacc cagggttca cctctctcc 780
 107 cctggaaagg acacc atg agc act gaa agc atg atc cgg gac gtg gag ctg 831
 108 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu
 109 1 5 10
 111 gcc gag gag gcg ctc ccc aag aag aca ggg ggg ccc cag ggc tcc agg 879
 112 Ala Glu Glu Ala Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg
 113 15 20 25
 115 cgg tgc ttg ttc ctc agc ctc ttc tcc ttc ctg atc gtg gca ggc gcc 927
 116 Arg Cys Leu Phe Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala
 117 30 35 40
 119 acc acg ctc ttc tgc ctg ctg cac ttt gga gtg atc ggc ccc cag agg 975
 120 Thr Thr Leu Phe Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg
 121 45 50 55 60
 123 gaa gag gtgagtgcct ggccagcctt catccactct cccacccaag gggaaatgag 1031
 124 Glu Glu
 126 agacgcaaga gagggagaga gatgggatgg gtgaaagatg tgcgctgata gggagggatg 1091
 128 agagagaaaa aaacatggag aaagacgggg atgcagaaag agatgtggca agagatgggg 1151
 130 aagagagaga gagaaagatg gagagacagg atgtctggca catggaagggt gctcactaag 1211
 132 tgtgtatgga gtgaatgaat gaatgaatga atgaacaagc agatatataa ataagatatg 1271

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133 gagacagatg tgggggtgtga gaagagagat gggggaagaa acaagtata tgaataaaga 1331
135 tgggtgagaca gaaagagcgg gaaatatgac agctaaggag agagatgggg gagataagga 1391
137 gagaagaaga taggggtgtct ggcacacaga agacactcag ggaaagagct gttgaatgct 1451
139 ggaaggtgaa tacacagatg aatggagaga gaaaaccaga cacctcaggg ctaagagcgc 1511
141 aggccagaca ggcagccagc tgttcctcct ttaaggggtga ctccctcgat gttaccatt 1571
143 ctcttctctc ccaacag ttc ccc agg gac ctc tct cta atc agc cct ctg 1621
144                               Phe Pro Arg Asp Leu Ser Leu Ile Ser Pro Leu
145                               65                               70
146 gcc cag gca gtc agtaagtgtc tccaaacctc tttcctaatt ctgggtttgg 1673
147 Ala Gln Ala Val
148                               75
150 gtttgggggt agggtagta cgggtatgga agcagtgagg gaaatttaaa gttttggtct 1733
152 tgggggagga tggatggagg tgaaagtagg ggggtatttt ctaggaagtt taagggtctc 1793
154 agctttttct tttctctctc ctcttca gga tca tct tct cga acc ccg agt gac 1847
155                               Arg Ser Ser Ser Arg Thr Pro Ser Asp
156                               80                               85
158 aag cct gta gcc cat gtt gta ggtaagagct ctgaggatgt gtcttggaaac 1898
159 Lys Pro Val Ala His Val Val
160                               90
161 ttggaggggt aggatttggg gattgaagcc cggtgatgg taggcagaac ttggagacaa 1958
163 tgtgagaagg actcgtgag ctcaagggaa ggggtggagga acagcacagg ccttagtggy 2018
165 atactcagaa cgtcatggcc aggtgggatg tgggatgaca gacagagagg acaggaaccg 2078
167 gatgtggggg ggcagagct cgagggccag gatgtggaga gtgaaccgac atggccacac 2138
169 tgactctcct ctccctctct cctccctcc a gca aac cct caa gct gag ggg 2190
170                               Ala Asn Pro Gln Ala Glu Gly
171                               95                               100
172 cag ctc cag tgg ctg aac cgc cgg gcc aat gcc ctc ctg gcc aat ggc 2238
173 Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly
174                               105                               110                               115
175 gtg gag ctg aga gat aac cag ctg gtg gtg cca tca gag ggc ctg tac 2286
176 Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr
177                               120                               125                               130
179 ctc atc tac tcc cag gtc ctc ttc aag ggc caa ggc tgc ccc tcc acc 2334
180 Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr
181                               135                               140                               145
183 cat gtg ctc ctc acc cac acc atc agc cgc atc gcc gtc tcc tac cag 2382
184 His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln
185                               150                               155                               160
187 acc aag gtc aac ctc ctc tct gcc atc aag agc ccc tgc cag agg gag 2430
188 Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu
189 165                               170                               175                               180
191 acc cca gag ggg gct gag gcc aag ccc tgg tat gag ccc atc tat ctg 2478
192 Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
193                               185                               190                               195
195 gga ggg gtc ttc cag ctg gag aag ggt gac cga ctc agc gct gag atc 2526
196 Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile
197                               200                               205                               210
199 aat cgg ccc gac tat ctc gac ttt gcc gag tct ggg cag gtc tac ttt 2574
200 Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe

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201          215          220          225
203 ggg atc att gcc ctg tga ggaggacgaa catccaacct tcccaaacgc 2622
204 Gly Ile Ile Ala Leu
205          230
206 ctccccctgcc ccaatccctt tattaccccc tccttcagac accctcaacc tcttctggct 2682
208 caaaaagaga attgggggct tagggtcgga acccaagctt agaactttaa gcaacaagac 2742
210 caccacttcg aaacctggga ttcaggaaatg tgtggcctgc acagtgaagt gctggcaacc 2802
212 actaagaatt caaactgggg cctccagaac tcaactggggc ctacagcttt gatccctgac 2862
214 atctggaatc tggagaccag ggagcctttg gttctggcca gaatgctgca ggacttgaga 2922
216 agacctcacc tagaaattga cacaagtgga ccttaggcct tcctctctcc agatgtttcc 2982
218 agaattcctt gagacacgga gccagccctt ccccatggag ccagctccct ctatttatgt 3042
220 ttgcacttgt gattatttat tatttattta ttatttattt atttacagat gaatgtattt 3102
222 atttgggaga ccgggggtatc ctgggggacc caatgtagga gctgccttgg ctcagacatg 3162
224 ttttcctgta aaacggagct gaacaatagg ctgttcccat gtageccctt ggcctctgtg 3222
226 ccttcttttg attatgtttt ttaaaatatt tatctgatta agttgtctaa acaatgctga 3282
228 tttggtgacc aactgtcact cattgctgag cctctgctcc ccaggggagt tgtgtctgta 3342
230 atgcacctac tattcagtgg cgagaaataa agtttgctta gaaaagaaac atggctctct 3402
232 tcttggaatt aattctgcat ctgcctcttc ttgtgggtgg gaagaagctc cctaagctct 3462
234 ctctccacag gctttaagat cctcgggacc cagtcctcct cttagactcc tagggcctct 3522
236 gagaccttac ataaacaaag cccaacagaa tattcccat ccccaggaa acaagagcct 3582
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240 <210> SEQ ID NO: 2
241 <211> LENGTH: 18
242 <212> TYPE: DNA
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Synthetic
248 <400> SEQUENCE: 2
249 catgctttca gtgctcat 18
251 <210> SEQ ID NO: 3
252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Synthetic
259 <400> SEQUENCE: 3
260 tgaaggagcg tctgctggct 20
262 <210> SEQ ID NO: 4
263 <211> LENGTH: 20
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Synthetic
270 <400> SEQUENCE: 4
271 gtgctcatgg tgcctttcc 20
273 <210> SEQ ID NO: 5
274 <211> LENGTH: 20
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence

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278 <220> FEATURE:
279 <223> OTHER INFORMATION: Synthetic
281 <400> SEQUENCE: 5
282 taatcacaag tgcaaacata 20
284 <210> SEQ ID NO: 6
285 <211> LENGTH: 20
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Synthetic
292 <400> SEQUENCE: 6
293 taaccccggtc tcccaaataa 20
295 <210> SEQ ID NO: 7
296 <211> LENGTH: 18
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Synthetic
303 <400> SEQUENCE: 7
304 agcaccgcct ggagccct 18
306 <210> SEQ ID NO: 8
307 <211> LENGTH: 20
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: Synthetic
314 <400> SEQUENCE: 8
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317 <210> SEQ ID NO: 9
318 <211> LENGTH: 20
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Synthetic
325 <400> SEQUENCE: 9
326 aqqcagaaga gcgtggtggc 20
328 <210> SEQ ID NO: 10
329 <211> LENGTH: 20
330 <212> TYPE: DNA
331 <213> ORGANISM: Artificial Sequence
333 <220> FEATURE:
334 <223> OTHER INFORMATION: Synthetic
336 <400> SEQUENCE: 10
337 aaagtgcagc aggcagaaga 20
339 <210> SEQ ID NO: 11
340 <211> LENGTH: 18
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:

VERIFICATION SUMMARY

DATE: 02/21/2002

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TIME: 12:39:06

Input Set : A:\EP.txt

Output Set: N:\CRF3\02212002\I824322B.raw

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L:682 M:283 W: Missing Blank Line separator, <220> field identifier
L:955 M:283 W: Missing Blank Line separator, <220> field identifier
L:1250 M:283 W: Missing Blank Line separator, <220> field identifier
L:1396 M:283 W: Missing Blank Line separator, <220> field identifier
L:2247 M:283 W: Missing Blank Line separator, <400> field identifier
L:6073 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
L:6084 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:503
L:6089 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4